

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
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Harley, Calvin
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- (ii) TITLE OF INVENTION: Novel Telomerase
- (iii) NUMBER OF SEQUENCES: 225
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(F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Apple, Randolph T.
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(C) REFERENCE/DOCKET NUMBER: 015389-002930US
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA 60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA 120
TCAAGCTGAT AATCATGGCA TTCCTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC 180
TAAACGTTG TACTCTTGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA 240
TTATAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTAATCCACG 300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360
AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA 420
TAGACAAAAA CTTCAATGAT TTGGATTTC AACTAAGGGA AATCAATTAG CAAAGACCCA 480
TTTATTAACA GCTCTTTCAA CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 540
TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600
GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 660
AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT 900
AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960
GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020
TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080
ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1140
GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1200
CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT 1260
TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC AAAAATTAT TGCTTGAGAA 1320
GATCAATACA AGAGAAATAT CATGGATGCA GGTGAGACC TCTGCAAAGC ATTTTTATTA 1380
TTTGTATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440

CGTCGTCTCG	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA	1500
AACCTATTAC	TACAGAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA	TCGCAGACTT	1560
AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT	GAAGAATGGA	AAAAGTCGCT	1620
TGGATTTGCA	CCTGGAAAAC	TCAGACTAAT	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	1680
GACTTTCAAT	AAGAAGATTG	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	1740
GAAGTTATTG	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC	1800
TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG	AGTTTGTTTG	1860
CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA	ACTATGGATA	TCGAAAAGTG	1920
ATATGATAGT	GTAAACAGAG	AAAAACTATC	AACATTCCCTA	AAAAC TACTA	AATTACTTTC	1980
TTCAGATTTT	TGGATTATGA	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	2040
TTGAAAAAC	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT	2100
TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAATG	AACAAAATGA	2160
CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA	AGAAATTATT	TTAAGAAAGA	2220
TAAC T TACTT	CAACCAGTCA	TTAATATTTG	CCAATATAAT	TACATTAACT	TTAATGGGAA	2280
GTTTTATAAA	CAAACAAAAG	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTCATC	2340
ATTTTATTAT	GCAACATTAG	AGGAAAGCTC	CTTAGGATTG	CTTAGAGATG	AATCAATGAA	2400
CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC	TTTTGATTAC	2460
AACTCAAGAG	AATAATGCAG	TATTGTTTTAT	TGAGAAACTT	ATAAACGTAA	GTCGTGAAAA	2520
TGGATTTAAA	TTCAATATGA	AGAAACTACA	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	2580
TGCAAAATAC	GGAATGGATA	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	2640
GATTGGCATC	TCAATTGATA	TGAAAAC TCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT	2700
AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT	CAATGTGGCT	2760
CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC	CATTATTTTA	GAAAGACGAT	2820
TACAACCGAA	GACTTTGCGA	ATAAACTCT	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	2880
ATACATGCAA	TGAGCCAAAG	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	2940
TATGATCGAC	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA	3000
CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG	ACTTTTTCCT	3060
TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA	AAGTACATTT	TCAACAGAGT	3120
TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	3180
TCAATATGAT	GCATAGTCGA	CTATTCTAAC	TTATTTTGGA	AAGTTAATTT	TCAATTTTTG	3240
TCTTATATAC	TGGGGTTTTTG	GGGTTTTGGG	GTTTTGGGG			3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
20 25 30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
85 90 95

Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
100 105 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
115 120 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
130 135 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
145 150 155 160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
165 170 175

Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
180 185 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
195 200 205

Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
210 215 220

Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
225 230 235 240

Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
245 250 255

His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
260 265 270

Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
275 280 285

Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
290 295 300

Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
305 310 315 320

Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
325 330 335

Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
340 345 350

Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
355 360 365

Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
370 375 380

Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
385 390 395 400

Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
405 410 415

Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
420 425 430

Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
435 440 445

Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
450 455 460

Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
485 490 495

Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
515 520 525

Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
530 535 540

Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
545 550 555 560

Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
565 570 575

Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
580 585 590

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
595 600 605

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
945 950 955 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
965 970 975

Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
995 1000 1005

Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
1010 1015 1020

Ser Leu Ile Gln Tyr Asp Ala
1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTTACAAC TGAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960

GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAT TTGTTGATTC TTCTGTAACC 1020
 GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC 1080
 TTAAAGATTT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG 1140
 TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTGTGA TTAGCTGGAA 1200
 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT 1260
 AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA 1320
 TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA 1380
 GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA 1440
 ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA 1500
 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA 1560
 TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT 1620
 ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA 1680
 GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT 1740
 TTGGGGTTTT GGGGTTTTGG GG 1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro	Gln	Asn	Pro	Lys	Thr	Pro	Lys	Pro	Leu	Lys	Lys	Lys	Lys	Leu	Arg
1				5					10					15	
Phe	Arg	Asn	Lys	Ile	Leu	Phe	Pro	His	Lys	Trp	Arg	Trp	Ile	Leu	Ile
			20					25					30		
Trp	Met	Ile	Lys	Ile	Tyr	Phe	Leu	Ile	His	Ser	Thr	Ser	Ile	Ala	Ala
			35				40					45			
Leu	Val	Val	Thr	Arg	Lys	Asp	Ala	Lys	His	Cys	Asn	Leu	Ala	Arg	Asn
			50			55					60				
Arg	Leu	His	Cys	Leu	Phe	Gln	Ser	Cys	Lys	Asn	Asn	Ser	Ser	Thr	Ser
65				70					75					80	
Arg	Met	Gln	Ile	Phe	Ile	Thr	Ile	Leu	Ser	Cys	Glu	Asn	Phe	Lys	Ala
				85				90						95	
Glu	Ser	Lys	Glu	Lys	Leu	Lys	His	Tyr	Cys	Leu	Asn	Lys	Ile	Arg	Cys
			100				105					110			
Gly	Leu	Phe	Tyr	Phe	Leu	Asp	His	Phe	Leu	Arg	Ser	Ile	Met	Glu	Lys

115					120					125					
Ile	Thr	Tyr	Lys	Val	Asn	Ser	Leu	Asp	Tyr	Phe	Pro	Ser	Gln	Gln	Cys
130					135					140					
Cys	Val	Tyr	Ile	His	Met	Arg	Met	Ser	Gln	Arg	Ile	Ser	Ile	His	Gln
145					150					155					160
Thr	Tyr	Gln	Arg	Gln	Thr	Arg	Tyr	Lys	Thr	Gln	Glu	Lys	Val	Cys	Ser
				165					170					175	
Asn	Ser	Arg	Arg	Thr	Tyr	Cys	Ile	Tyr	Tyr	Ser	Tyr	Gly	Phe	Tyr	Tyr
				180				185					190		
Asn	Cys	Phe	Arg	Tyr	Arg	Arg	Cys	Thr	Pro	Glu	Ser	Cys	Asp	Asn	Cys
		195					200					205			
Lys	Ser	Cys	Leu	Gln	Leu	Lys	Glu	Ser	Gln	Phe	Cys	Lys	Phe	Cys	Val
	210					215					220				
Cys	His	Tyr	Phe	Val	Asn	Ser	Gln	Ile	Ser	Tyr	Leu	Asn	Leu	Met	Asp
225					230					235					240
Ser	Tyr	Arg	Asn	Lys	Pro	Asn	Lys	Pro	Cys	Lys	Phe	Asn	Gly	Ile	Tyr
				245					250					255	
Val	Lys	Ser	Phe	Gly	Thr	Asn	Ala	His	Cys	Ile	Tyr	Ile	Gly	Phe	Leu
			260					265					270		
Lys	His	Arg	Tyr	Thr	Glu	Cys	Phe	Arg	Asp	Cys	Phe	Ser	Leu	Gln	Gln
		275					280					285			
Ile	Thr	Cys	Phe	Asp	Tyr	Ser	Cys	Ser	Ser	Leu	Ile	Ser	Leu	Lys	Glu
	290					295					300				
Ala	Gly	Glu	Met	Lys	Arg	Arg	Leu	Lys	Lys	Glu	Ile	Ser	Lys	Phe	Val
305					310					315					320
Asp	Ser	Ser	Val	Thr	Gly	Ile	Asn	Asn	Lys	Asn	Ile	Ser	Asn	Glu	Lys
				325					330					335	
Glu	Glu	Glu	Leu	Ser	Gln	Ser	Cys	Phe	Leu	Lys	Ile	Ser	Lys	Ile	Pro
			340					345					350		
Gly	Lys	Arg	Asp	Thr	Phe	Ile	Lys	Ile	His	Ile	Leu	Phe	Phe	Ile	Ser
		355					360					365			
Gln	Leu	Leu	Phe	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Phe	Asp	Leu	Glu	Val
	370					375					380				
Lys	Ser	Ile	Lys	Glu	Lys	Arg	Thr	Glu	Val	Thr	Leu	Ile	His	Ile	His
385					390					395					400
Arg	Ser	Thr	Phe	Ile	Tyr	Pro	Ile	Arg	Cys	Gly	Asn	Ser	Ser	His	Pro
				405					410					415	
Phe	Lys	Cys	Tyr	Glu	Asp	Ile	Phe	Arg	Val	Lys	Lys	Trp	Ser	Arg	Asn
			420					425					430		
Leu	Asn	Gln	Lys	Glu	Leu	Arg	Arg	Tyr	Cys	Lys	Arg	Ile	Glu	Leu	Ile
		435					440					445			

Phe Arg Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Arg Gly Asn Cys
 450 455 460
 Thr Glu Asp His Arg Asn Lys Val Thr Phe Ile Asn Arg Ile Asn Ile
 465 470 475 480
 Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys Lys Leu Asn Ser
 485 490 495
 Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu
 500 505 510
 Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln Ile Lys Cys Val Gln Lys
 515 520 525
 Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu Lys Arg Gly
 530 535 540
 Val Leu Gly Phe Trp Gly Phe Gly
 545 550

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys
 1 5 10 15
 Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr
 20 25 30
 Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser Tyr Ile Gln Gln Val Gln
 35 40 45
 Leu Leu Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala
 50 55 60
 Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu
 65 70 75 80
 Gly Cys Lys Ser Leu Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys
 85 90 95
 Arg Arg Ala Lys Ser Arg Asn Cys Asn Ile Thr Asn Val Ile Lys Ser
 100 105 110
 Gly Asn Glu Asp Tyr Ser Ile Phe Ile Thr Ser Gly Ala Leu Trp Arg
 115 120 125
 Lys Leu Leu Asn Thr Lys Arg Thr Val Trp Ile Ile Ser Leu Ala Asn
 130 135 140
 Asn Asp Glu Tyr Ile Lys Phe Ile Cys Glu Cys Val Lys Gly Ser Arg
 145 150 155 160

Tyr Ile Arg Leu Thr Lys Asp Lys Leu Ala Ile Lys Arg Lys Lys Lys
 165 170 175
 Phe Asp Asn Arg Thr Ala Glu Glu Leu Ile Ala Phe Thr Ile Arg Met
 180 185 190
 Gly Phe Ile Thr Ile Val Leu Gly Ile Asp Gly Glu Leu Pro Ser Leu
 195 200 205
 Glu Thr Ile Glu Lys Ala Val Tyr Asn Cys Arg Asn Arg Ser Ser Glu
 210 215 220
 Ser Ser Asp Val Tyr Ala Ile Ile Leu Cys Ile Asn Leu Lys Tyr Leu
 225 230 235 240
 Ile Ser Ile Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser
 245 250 255
 Leu Met Glu Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe
 260 265 270
 Ile Leu Asp Ser Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu
 275 280 285
 Ala Tyr Asn Arg Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr
 290 295 300
 Leu Lys Lys Gln Ala Lys Cys Lys Glu Asp Arg Lys Arg Phe Gln Asn
 305 310 315 320
 Leu Leu Ile Leu Leu Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys
 325 330 335
 Lys Lys Lys Ser Tyr His Asn Pro Asp Ser Arg Phe Gln Lys Phe Gln
 340 345 350
 Val Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe
 355 360 365
 His Ser Cys Tyr Phe Leu Leu Ser Gln Tyr Phe Leu Ile Ser Trp Lys
 370 375 380
 Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg Leu Ser Leu Phe Thr
 385 390 395 400
 Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu Thr Ala
 405 410 415
 Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu Glu Ser
 420 425 430
 Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp Ile Ala
 435 440 445
 Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln Ser Cys
 450 455 460
 Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile Lys Glu
 465 470 475 480
 Ile Lys Leu Leu Leu Ile Arg Glu Thr Lys Leu Leu Ile Arg Ser Ala
 485 490 495

Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg Gln Lys Ile
500 505 510

Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser Gln Lys
515 520 525

Lys Lys Gly Asn Lys Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu
530 535 540

Phe Phe Ser Ile Ile Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val
545 550 555 560

Leu Gly

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
1 5 10 15

Val Val Lys Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu
20 25 30

Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser
35 40 45

Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys
50 55 60

Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr
65 70 75 80

Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val
85 90 95

Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe
100 105 110

Lys Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys
115 120 125

Glu His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly
130 135 140

Leu Phe Pro Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu
145 150 155 160

Ser Lys Asp Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu Asn
165 170 175

Ala Arg Lys Ser Leu Ile Ile Glu Gln Lys Asn Leu Leu His Leu
180 185 190

Leu	Phe	Val	Trp	Val	Leu	Leu	Gln	Leu	Phe	Val	Ser	Thr	Val	Asn	Ser
		195					200						205		
Arg	Val	Leu	Arg	Gln	Leu	Lys	Lys	Leu	Phe	Thr	Thr	Glu	Gly	Ile	Ala
	210					215					220				
Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu	Phe	Cys	Glu	Leu	Ile	Ser
225					230					235					240
Asn	Ile	Leu	Ser	Gln	Phe	Asn	Gly	Leu	Lys	Gln	Thr	Lys	Thr	Met	Gln
				245					250					255	
Val	Trp	Asn	Ile	Arg	Ile	Leu	Trp	Asp	Lys	Cys	Thr	Leu	Asn	Leu	Tyr
			260					265					270		
Trp	Ile	Leu	Lys	Ala	Ile	His	Arg	Met	Leu	Arg	Leu	Ile	Leu	Thr	Thr
	275						280					285			
Asp	Tyr	Leu	Phe	Cys	Leu	Leu	Leu	Leu	Ile	Ser	Tyr	Ile	Phe	Lys	Arg
	290					295					300				
Ser	Arg	Arg	Asn	Glu	Lys	Lys	Thr	Lys	Glu	Arg	Asp	Phe	Lys	Ile	Cys
305					310					315					320
Cys	Phe	Phe	Cys	Asn	Arg	Asn	Gln	Gln	Glu	Tyr	Gln	Arg	Lys	Arg	Arg
				325					330					335	
Arg	Ala	Ile	Thr	Ile	Leu	Ile	Leu	Lys	Asp	Phe	Lys	Asn	Ser	Arg	Glu
			340					345					350		
Arg	Tyr	Ile	His	Asn	Ser	Tyr	Ile	Ile	Val	Phe	His	Phe	Thr	Ala	Val
		355					360					365			
Ile	Phe	Phe	Tyr	Leu	Asn	Asn	Ile	Phe	Cys	Leu	Ala	Gly	Ser	Lys	Lys
	370					375					380				
Tyr	Gln	Ile	Arg	Glu	Ala	Leu	Asp	Cys	Gly	Asn	Leu	Ala	Tyr	Ser	His
385					390					395					400
Ser	Ile	Asp	Leu	His	Ile	Ser	Asn	Thr	Met	Ile	Arg	Lys	Gln	Gln	Ser
				405					410					415	
Ser	Val	Leu	Lys	Ile	Val	Leu	Cys	Gly	Leu	Asn	Phe	Ser	Gln	Glu	Met
			420					425					430		
Glu	Pro	Lys	Ser	Ser	Lys	Arg	Ile	Ala	Ser	Ile	Leu	Gln	Lys	Asn	Arg
		435					440					445			
Thr	Leu	Asn	Leu	Ser	Leu	Ile	Ser	Ile	Thr	Asn	Leu	Asp	Cys	Leu	Lys
	450					455					460				
Arg	Leu	Thr	Arg	Gln	Leu	His	Arg	Arg	Ser	Leu	Lys	Lys	Ser	Asn	Phe
465					470					475					480
Tyr	Leu	Glu	Asn	Lys	Leu	Asn	Tyr	Tyr	Arg	Asp	Gln	Arg	Ser	Ser	Ile
				485					490					495	
Asp	Glu	Ile	Lys	Ala	Glu	Leu	Lys	Leu	Asp	Asn	Lys	Lys	Tyr	Lys	Pro
			500					505					510		
Trp	Ser	Lys	Tyr	Cys	Gly	Arg	Lys	Arg	Arg	Pro	Val	Ser	Lys	Arg	Lys
		515					520					525			

Asn Lys Ala Ile Asn Lys Met Ser Thr Glu Val Lys Lys Lys Ile Tyr
530 535 540

Phe Phe Gln Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Ile	Glu	Asn	Asn	Gln	Ala	Gln	Gln	Pro	Lys	Ala	Glu	Lys	Leu	1	5	10	15
Trp	Trp	Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	20	25	30	
Val	Arg	Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	35	40	45	
Ala	Ala	Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	50	55	60	
Arg	Arg	Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	65	70	75	80
Pro	Glu	Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	85	90	95	
Ile	Arg	Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	100	105	110	
Asn	Thr	Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	115	120	125	
Pro	Asn	Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	130	135	140	
Phe	Asp	Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	145	150	155	160
Gln	Asp	Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	165	170	175	
Val	Arg	Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	180	185	190	
Cys	Thr	Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	195	200	205	
Thr	Asn	Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	210	215	220	
Leu	Leu	Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	225	230	235	240

Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
245 250 255

Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
260 265 270

Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
275 280 285

Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
290 295 300

Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
305 310 315 320

Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
325 330 335

Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
340 345 350

Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
355 360 365

Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
370 375 380

Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
385 390 395 400

Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
405 410 415

Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
420 425 430

Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
435 440 445

Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
450 455 460

Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
465 470 475 480

Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
485 490 495

Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
500 505 510

Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
515 520 525

Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
530 535 540

Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
545 550 555 560

Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
565 570 575

Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
805 810 815

Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
835 840 845

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp
865 870

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn
1 5 10 15

Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys
20 25 30

Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln
35 40 45

Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu
50 55 60

Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr
65 70 75 80

Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
1 5 10 15

Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
20 25 30

Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys
35 40 45

Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln
50 55 60

Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His
65 70 75 80

Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys
85 90 95

Ala Phe Ile Leu
100

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1 5 10 15

Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
20 25 30

Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
35 40 45

Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
50 55 60

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu
65 70 75 80

Ile Glu Thr Leu Leu
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile
1 5 10 15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr
20 25 30

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
35 40 45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
50 55 60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Lys Cys Tyr
65 70 75 80

Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys
85 90 95

Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1 5 10 15

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20 25 30

Leu Leu Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
35 40 45

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser
50 55 60

Ser Leu Gly Phe Leu
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15

Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30

Ile Asn Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser
35 40 45

Leu Ser Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln
 50 55 60

Leu His Asn Asp Arg
 65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
 1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30

Ser Asp His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro
 35 40 45

Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg
 50 55 60

Leu Ala Gly Leu Ala
 65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
 1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
 20 25 30

Ile Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys
 35 40 45

Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro
 50 55 60

Phe Arg Lys Gln Asn
 65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
20 25 30
Lys Asn Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
35 40 45
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe
50 55 60
Tyr Ser Glu Phe Lys
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1 5 10 15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
20 25 30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Gln Asp Tyr Cys Asp
35 40 45
Trp Ile Gly Ile Ser Ile
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
1 5 10 15
Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
20 25 30
Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr Lys Cys Leu Tyr Lys
35 40 45
Tyr Leu Gly Phe Gln Gln
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15
Asn Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly
20 25 30
Leu Thr Ile Asn Glu Glu Lys Thr Leu Ile Glu Thr Pro Ala Arg Phe
35 40 45
Leu Gly Tyr Asn Ile
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
1 5 10 15
Gly His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp
20 25 30
Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu
35 40 45
Trp Met Gly Tyr Glu Leu
50

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
20 25 30
Asn Ala Lys Ala Asn Arg Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
1 5 10 15
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
20 25 30
Glu Ile Glu Thr Leu Leu Met
35

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Cys His Gln Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg Asp
1 5 10 15
Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro Leu
20 25 30
Glu Ile Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1 5 10 15
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
20 25 30
Leu Glu Thr Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg
1 5 10 15
Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val
20 25 30
Pro Leu Ser Val Leu Val Thr
35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr
1 5 10 15
Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro
20 25 30
Ile Ser Thr Ile Ala Thr
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA 60

ACTCCACGAA AGTGGAGTAA GTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CCAAACCCC AAAACCCCA CAGGGGTTTT GGGGTTTTGG GTTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAACCCC AAAACCCCA AACCCCA GGGGTTTTGG GTTTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA	60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA AATGGAAATT GAAAACAACT AAGCACAATA	120
GCCAAAAGCC GAAAAATTGT GGTGGGAACT TGAATTAGAG ATGCAAGAAA ACCAAAATGA	180
TATATAAGTT AGGGTTAAGA TTGACGATCC TAAGCAATAT CTCGTGAACG TCACTGCAGC	240
ATGTTTGTGT TAGGAAGGTA GTTACTACTA AGATAAAGAT GAAAGAAGAT ATATCATCAC	300
TAAAGCACTT CTTGAGGTGG CTGAGTCTGA TCCTGAGTTC ATCTGCTAGT TGGCAGTCTA	360
CATCCGTAAT GAACTTTACA TCAGAACTAC CACTAACTAC ATTGTAGCAT TTTGTGTTGT	420
CCACAAGAAT ACTCAACCAT TCATCGAAAA GTACTTCAAC AAAGCAGTAC TTTTGCCTAA	480
TGACTTACTG GAAGTCTGTG AATTTGCATA GGTTCCTCTAT ATTTTGTATG CAACTGAATT	540
CAAAAATTTG TATCTTGATA GGATACTTTC ATAAGATATT CGTAAGGAAC TCACTTTCCG	600
TAAGTGTTTA CAAAGATGCG TCAGAAGCAA GTTTTCTGAA TTCAACGAAT ACTAACTTGG	660
TAAGTATTGC ACTGAATCCT AACGTAAGAA AACAATGTTC CGTTACCTCT CAGTTACCAA	720
CAAGTAAAAG TGGGATTAAA CTAAGAAGAA GAGAAAAGAG AATCTCTTAA CCAAACTTTA	780
GGCAATAAAG GAATCTGAAG ATAAGTCCAA GAGAGAACT GGAGACATAA TGAACGTTGA	840
AGATGCAATC AAGGCTTTAA AACCAGCAGT TATGAAGAAA ATAGCCAAGA GATAGAATGC	900
CATGAAGAAA CACATGAAGG CACCTAAAAT TCCTAACTCT ACCTTGGAAT CAAAGTACTT	960
GACCTTCAAG GATCTCATT AGTTCTGCCA TATTTCTGAG CCTAAAGAAA GAGTCTATAA	1020
GATCCTTGGT AAAAAATACC CTAAGACCGA AGAGGAATAC AAAGCAGCCT TTGGTGATTC	1080
TGCATCTGCA CCCTTCAATC CTGAATTGGC TGGAAAGCGT ATGAAGATTG AAATCTCTAA	1140
AACATGGGAA AATGAACTCA GTGCAAAAGG CAACACTGCT GAGGTTTGGG ATAATTTAAT	1200
TTCAAGCAAT TAACTCCCAT ATATGGCCAT GTTACGTAAC TTGTCTAACA TCTTAAAAGC	1260
CGGTGTTTCA GATACTACAC ACTCTATTGT GATCAACAAG ATTTGTGAGC CCAAGGCCGT	1320
TGAGAACTCC AAGATGTTCC CTCTTCAATT CTTTAGTGCC ATTGAAGCTG TTAATGAAGC	1380
AGTTACTAAG GGATTCAAGG CCAAGAAGAG AGAAAATATG AATCTTAAAG GTCAAATCGA	1440
AGCAGTAAAG GAAGTTGTTG AAAAAACCGA TGAAGAGAAG AAAGATATGG AGTTGGAGTA	1500

AACCGAAGAA GGAGAATTTG TTAAAGTCAA CGAAGGAATT GGCAAGCAAT ACATTAAGTC 1560
 CATTGAACTT GCAATCAAGA TAGCAGTTAA CAAGAATTTA GATGAAATCA AAGGACACAC 1620
 TGCAATCTTC TCTGATGTTT CTGGTTCTAT GAGTACCTCA ATGTCAGGTG GAGCCAAGAA 1680
 GTATGGTTCC GTTCGTACTT GTCTCGAGTG TGCATTAGTC CTTGGTTTGA TGGTAAAATA 1740
 ACGTTGTGAA AAGTCCTCAT TCTACATCTT CAGTTCACCT AGTTCTCAAT GCAATAAGTG 1800
 TTACTTAGAA GTTGATCTCC CTGGAGACGA ACTCCGTCCT TCTATGTAAA AACTTTTGCA 1860
 AGAGAAAGGA AAAC TTGGTG GTGGTACTGA TTTCCCTAT GAGTGCATTG ATGAATGGAC 1920
 AAAGAATAAA ACTCACGTAG ACAATATCGT TATTTTGTCT GATATGATGA TTGCAGAAGG 1980
 ATATTCAGAT ATCAATGTTA GAGGCAGTTC CATTGTTAAC AGCATCAAAA AGTACAAGGA 2040
 TGAAGTAAAT CCTAACATTA AAATCTTTGC AGTTGACTTA GAAGGTTACG GAAAGTGCCT 2100
 TAATCTAGGT GATGAGTTCA ATGAAAACAA CTACATCAAG ATATTCGGTA TGAGCGATTC 2160
 AATCTTAAAG TTCATTTTCA CCAAGCAAGG AGGAGCAAAT ATGGTCGAAG TTATCAAAAA 2220
 CTTTGCCCTT CAAAAAATAG GACAAAAGTG AGTTTCTTGA GATTCTTCTA TAACAAAAAT 2280
 CTCACCCAC TTTTTTGTTC TATTGCATAG CCATTATGAA ATTTAAATTA TTATCTATTT 2340
 ATTTAAGTTA CTTACATAGT TTATGTATCG CAGTCTATTA GCCTATTCAA ATGATTCTGC 2400
 AAAGAACAAA AAAGATTAAA A 2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg
 1 5 10 15
 Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala
 20 25 30
 Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg
 35 40 45
 Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu
 50 55 60
 Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg
 65 70 75 80
 Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys Asn Thr
 85 90 95

\vec{B}	\vec{B}	\vec{B}	\vec{B}
$\frac{\partial \Phi}{\partial t} > 0$	$\frac{\partial \Phi}{\partial t} < 0$	$\frac{\partial \Phi}{\partial t} > 0$	$\frac{\partial \Phi}{\partial t} < 0$
\vec{E}	\vec{E}	\vec{E}	\vec{E}
\vec{v}	\vec{v}	\vec{v}	\vec{v}

Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540
 Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly
 545 550 555 560
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys
 565 570 575
 Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr
 580 585 590
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met
 595 600 605
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val
 610 615 620
 Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile
 625 630 635 640
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp
 645 650 655
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser
 660 665 670
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu
 675 680 685
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly
 690 695

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2829 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAAAA GCAAACTACA AAGAAAATGT CAAGGCGTAA	60
CTAAAAAAAAAG CCATAGGCTC CTATAGGCAA TGAAACAAAT CTTGATTTTG TATTACAAAA	120
TCTAGAAGTT TACAAAAGCC AGATTGAGCA TTATAAGACC TAGTAGTAAT AGATCAAAGA	180
GGAGGATCTC AAGCTTTTAA AGTTCAAAAA TTAAGATTAG GATGGAAACT CTGGCAACGA	240
TGATGATGAT GAAGAAAACA ACTCAAATAA ATAATAAGAA TTATTAAGGA GAGTCAATTA	300
GATTAAGTAG CAAGTTTAAT TGATAAAAAA AGTTGGTTCT AAGGTAGAGA AAGATTTGAA	360
TTTGAACGAA GATGAAAAACA AAAAGAATGG ACTTTCAGAA TAGCAAGTGA AAGAAGAGTA	420
ATTAAGAACG ATTACTGAAG AATAGGTTAA GTATTAAAT TTAGTATTTA ACATGGACTA	480
CCAGTTAGAT TTAAATGAGA GTGGTGGCCA TAGAAGACAC AGAAGAGAAA CAGATTATGA	540
TACTGAAAAA TGGTTTGAAA TATCTCATGA CCAAAAAAT TATGTATCAA TTTACGCCAA	600
CTAAAAGACA TCATATTGTT GGTGGCTTAA AGATTATTTT AATAAAAACA ATTATGATCA	660
TCTTAATGTA AGCATTAACA GACTAGAAAC TGAAGCCGAA TTCTATGCCT TTGATGATTT	720
TTCAACAAACA ATCAAACTTA CTAATAATTC TTACTAGACT GTTAACATAG ACGTTAATTT	780
TGATAATAAT CTCTGTATAC TCGCATTGCT TAGATTTTAA TTATCACTAG AAAGATTCAA	840
TATTTTGAAT ATAAGATCTT CTTATACAAG AAATTAATAT AATTTTGAGA AAATTGGTGA	900
GCTACTTGAA ACTATCTTCG CAGTTGTCTT TTCTCATCGC CACTTACAAG GCATTCATTT	960
ACAAGTTCCT TCGGAAGCGT TCTAATATTT AGTTAACTCC TCATCATAAA TTAGCGTTAA	1020
AGATAGCTAA TTATAGGTAT ACTCTTCTC TACAGACTTA AAATTAGTTG AACTAACAA	1080
AGTCCAAGAT TATTTTAAGT TCTTATAAGA ATCCCTCGT TTGACTCATG TAAGCTAGTA	1140
GGCTATCCCA GTTAGTGCTA CTAACGCTGT AGAGAACCTC AATGTTTTAC TTAAAAAGGT	1200
CAAGCATGCT AATCTTAATT TAGTTTCTAT CCCTACCTAA TTCAATTTTG ATTTCTACTT	1260
TGTTAATTTA TAACATTTGA AATTAGAGTT TGGATTAGAA CCAAATATTT TGACAAAAACA	1320
AAAGCTTGAA AATCTACTTT TGAGTATAAA ATAATCAAAA AATCTTAAAT TTTTAAGATT	1380
AACTTTTAC ACCTACGTTG CTTAAGAAAC CTCCAGAAAA CAGATATTAA AACAAGCTAC	1440
AACAATCAAA AATCTCAAAA ACAATAAAAA TCAAGAAGAA ACTCCTGAAA CTAAAGATGA	1500
AACTCCAAGC GAAAGCACAA GTGGTATGAA ATTTTTTGAT CATCTTCTG AATTAACCGA	1560
GCTTGAAGAT TTCAGCGTTA ACTTGTAAGC TACCCAAGAA ATTTATGATA GCTTGCACAA	1620

ACTTTTGATT AGATCAACAA ATTTAAAGAA GTTCAAATTA AGTTACAAAT ATGAAATGGA 1680
AAAGAGTAAA ATGGATACAT TCATAGATCT TAAGAATATT TATGAAACCT TAAACAATCT 1740
TAAAAGATGC TCTGTTAATA TATCAAATCC TCATGGAAAC ATTTCTTATG AACTGACAAA 1800
TAAAGATTCT ACTTTTTATA AATTTAAGCT GACCTTAAAC TAAGAATTAT AACACGCTAA 1860
GTATACTTTT AAGTAGAACG AATTTTAATT TAATAACGTT AAAAGTGCAA AAATTGAATC 1920
TTCCTCATT A GAAAGCTTAG AAGATATTGA TAGTCTTTGC AAATCTATTG CTTCTTGTA 1980
AAATTTACAA AATGTTAATA TTATCGCCAG TTTGCTCTAT CCCAACAATA TTTAGAAAAA 2040
TCCTTTCAAT AAGCCCAATC TTCTATTTTT CAAGCAATTT GAATAATTGA AAAATTTGGA 2100
AAATGTATCT ATCAACTGTA TTCTTGATCA GCATATACTT AATTCTATTT CAGAATTCTT 2160
AGAAAAGAAT AAAAAAATAA AAGCATTCTT TTTGAAAAGA TATTATTTAT TACAATATTA 2220
TCTTGATTAT ACTAAATTAT TTAAACACT TCAATAGTTA CCTGAATTAA ATTAAGTTTA 2280
CATTAAATTAG CAATTAGAAG AATTGACTGT GAGTGAAGTA CATAAGTAAG TATGGGAAAA 2340
CCACAAGCAA AAAGCTTTCT ATGAACCATT ATGTGAGTTT ATCAAAGAAT CATCCTAAAC 2400
CCTTTAGCTA ATAGATTTTG ACCAAAACAC TGTAAGTGAT GACTCTATTA AAAAGATTTT 2460
AGAATCTATA TCTGAGTCTA AGTATCATCA TTATTTGAGA TTGAACCCTA GTTAATCTAG 2520
CAGTTTAATT AAATCTGAAA ACGAAGAAAT TTAAGAACTT CTCAAAGCTT GCGACGAAAA 2580
AGGTGTTTTA GTAAAAGCAT ACTATAAATT CCCTCTATGT TTACCAACTG GTACTTATTA 2640
CGATTACAAT TCAGATAGAT GGTGATTAAT TAAATATTAG TTTAAATAAA TATTAAATAT 2700
TGAATATTTT TTTGCTTATT ATTTGAATAA TACATACAAT AGTCATTTTT AGTGTTTTGA 2760
ATATATTTTA GTTATTTAAT TCATTATTTT AAGTAAATAA TTATTTTCA ATCATTTTTT 2820
AAAAAATCG 2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ser	Arg	Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	Pro	Ile	Gly	Asn	Glu
1				5				10					15		
Thr	Asn	Leu	Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	Val	Tyr	Lys	Ser	Gln
		20					25					30			
Ile	Glu	His	Tyr	Lys	Thr	Gln	Gln	Gln	Ile	Lys	Glu	Glu	Asp	Leu	
	35					40					45				

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
50 55 60
Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
65 70 75 80
Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
85 90 95
Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
100 105 110
Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
115 120 125
Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
130 135 140
Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
145 150 155 160
Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
165 170 175
Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
180 185 190
Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
195 200 205
Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
210 215 220
Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
225 230 235 240
Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
245 250 255
Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
260 265 270
Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
275 280 285
Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
290 295 300
Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
305 310 315 320
Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
325 330 335
Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
340 345 350
Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
355 360 365
Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
370 375 380

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
 500 505 510
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
 515 520 525
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
 530 535 540
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
 625 630 635 640
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
 705 710 715 720
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880
 His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
 1 5 10 15
 Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
 20 25 30
 Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
 1 5 10 15
 Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
 20 25 30
 Pro Asn Val Asn Leu Leu Met Arg Leu Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "RNA"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 - (B) LOCATION: 12..25
 - (D) OTHER INFORMATION: /mod_base= OTHER
- /note= "The residues located at these positions are 2-O-methylribonucleoti..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAGACCTGTT AGGUUUUGGG GUUUUG

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTTG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST) AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGCCTGGCT GATGAGTGTG TACGTCGTCG AGCTGCTCAG GTCTTTCTTT 60
TATGTCACGG AGACCACGTT TCAAAAGAAC AGGCTCTTTT TCTACCGGAA GAGTGTCTGG 120
AGCAAGTTGC AAAGCATTTG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG 180
TCGGAAGCAG AGGTCAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC 240
CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA 300
GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCACTG 360
TTCAGCGTGC TCAACTACGA GCGGGCGCG 389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys
1 5 10 15
Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe
20 25 30

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
 35 40 45
 Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
 50 55 60
 Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
 65 70 75 80
 Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
 85 90 95
 Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
 100 105 110
 Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
 115 120 125
 Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 130 135 140
 Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
 145 150 155 160
 Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175
 Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190
 Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205
 Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220
 Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
 1 5 10 15

His	Asn	Phe	Glu 20	Asn	Leu	Asn	Gln	Leu 25	Ala	Ile	Cys	Phe	Ile 30	Ser	Trp
Leu	Phe	Arg 35	Gln	Leu	Ile	Pro	Lys 40	Ile	Ile	Gln	Thr	Phe 45	Phe	Tyr	Cys
Thr	Glu 50	Ile	Ser	Ser	Thr	Val 55	Thr	Ile	Val	Tyr	Phe 60	Arg	His	Asp	Thr
Trp 65	Asn	Lys	Leu	Ile	Thr 70	Pro	Phe	Ile	Val	Glu 75	Tyr	Phe	Lys	Thr	Tyr 80
Leu	Val	Glu	Asn	Asn 85	Val	Cys	Arg	Asn	His 90	Asn	Ser	Tyr	Thr	Leu 95	Ser
Asn	Phe	Asn	His 100	Ser	Lys	Met	Arg	Ile 105	Ile	Pro	Lys	Lys	Ser 110	Asn	Asn
Glu	Phe	Arg 115	Ile	Ile	Ala	Ile	Pro 120	Cys	Arg	Gly	Ala	Asp 125	Glu	Glu	Glu
Phe	Thr 130	Ile	Tyr	Lys	Glu	Asn 135	His	Lys	Asn	Ala	Ile 140	Gln	Pro	Thr	Gln
Lys 145	Ile	Leu	Glu	Tyr	Leu 150	Arg	Asn	Lys	Arg	Pro 155	Thr	Ser	Phe	Thr	Lys 160
Ile	Tyr	Ser	Pro	Thr 165	Gln	Ile	Ala	Asp	Arg 170	Ile	Lys	Glu	Phe	Lys 175	Gln
Arg	Leu	Leu	Lys 180	Lys	Phe	Asn	Asn	Val 185	Leu	Pro	Glu	Leu	Tyr 190	Phe	Met
Lys	Phe	Asp 195	Val	Lys	Ser	Cys	Tyr 200	Asp	Ser	Ile	Pro	Arg 205	Met	Glu	Cys
Met	Arg 210	Ile	Leu	Lys	Asp	Ala 215	Leu	Lys	Asn	Glu	Asn 220	Gly	Phe	Phe	Val
Arg 225	Ser	Gln	Tyr	Phe	Phe 230	Asn	Thr	Asn							

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) **FEATURE:**

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..233
(D) OTHER INFORMATION: /note= "TRT motifs from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT	120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG	300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT	420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GGCGCCCAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCTCTTC	600
TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTCCCA CAAATTGGT TAAAATTCCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT	780
GAATAGTATT TGCCCACCAT TGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAATTATC AAGAATCTAA ATCTTTTATT	960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAAGT TAAGATTAAA	1020
GGATTTTCGG TGGTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT	1080
GAATCAATTG GCGATTTGTT TCATTTTCCTG GCTATTTAGA CAACTAATTC CAAAATTAT	1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA	1200
TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT	1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA	1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTTCAGG ATTATTGCCA TCCCATGCAG	1380
AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC	1440
CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAGGCCG ACTAGTTTTA CTAAAATATA	1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT	1560
TAATAATGTC TTACCAGAGC TTTATTTTCA GAAATTTGAT GTCAAATCTT GCTATGATTC	1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT	1680
TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT	1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT	1800

TEATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT 1860
 GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTGAGGGCT CTAGTTTATC 1920
 TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC 1980
 CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCCTTA TAATATCAAC 2040
 AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GCGGATTTT AAAAATATAA 2100
 TCGGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT 2160
 TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGA AACATTCAAG 2220
 CACAATGAAT AATTTCCATA TCCGTTTCGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAT 2280
 AGCGCTGTTT AACACTAGAA TCTCTTATAA AACAATTGAC ACAAATTTAA ATTCAACAAA 2340
 CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC 2400
 TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTCGT TCTTACAACG 2460
 CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA 2520
 TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA 2580
 ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C 2631

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 1 5 10 15
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 20 25 30
 Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 35 40 45
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 50 55 60
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 65 70 75 80

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
85 90 95
Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
100 105 110
Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
115 120 125
Ala

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595..1857, 1894..2286, 2326..2396, 2436..2705, 2746..2862, 2914..3083, 3125..3309, 3356..3504, 3546..3759, 3797..4046, 4086..4252, 4296..4392, 4435..4597)
- (D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe telomerase catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTCTG	240
GGTTCGCTTA CTTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780

TSTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA 840
 AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA 900
 TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC 958
 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG 1006
 Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
 1 5 10 15
 AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT 1054
 Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
 20 25 30
 TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG 1102
 Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
 35 40 45
 AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA 1150
 Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
 50 55 60
 GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
 Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
 65 70 75 80
 AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTCT 1246
 Lys Cys Ser Gln Ser Glu
 85
 ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG 1299
 Leu Ile Ala Asn Val Val Lys Gln Met
 90 95
 TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT 1347
 Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe
 100 105 110
 TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTCAAAGA 1403
 Ser Met
 GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA 1454
 Asn His Glu Asp Phe Arg Ala Met His Val
 115 120
 AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA 1502
 Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile
 125 130 135
 TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT 1543
 Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile
 140 145 150
 GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC 1598
 Ile
 GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG 1646
 Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu
 155 160 165 170

GET CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAAC TAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC Glu Ile Ile Leu Lys 370 Asp	2327
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys	2426

390	395	
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA		2474
Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser		
400	405	
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT		2522
Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe		
410	415	420
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA		2570
Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu		
425	430	435 440
CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT		2618
Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr		
445	450	455
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT		2666
Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile		
460	465	470
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA		2715
Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu		
475	480	485
GTATTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG		2769
Asn Asn Val Arg Met Asp Thr Gln		
490		
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT		2817
Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn		
495	500	505
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG		2862
Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys		
510	515	520
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT		2919
Met Gly		
525		
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG		2967
Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val		
530	535	540
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA		3015
Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro		
545	550	555
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT		3063
Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu		
560	565	570
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT		3113
Leu Lys His Arg Met Phe Gly		
575	580	
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC		3161
Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser		
585	590	

TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTSTA ACAAATTCCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATACCAAT TGTTGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu	3942

	800	805	810	
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT				3990
Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser	815	820	825	
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA				4038
Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys	830	835	840	
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG				4089
Ile Leu Arg Ser	845			
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA				4137
Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser	850	855	860	
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT				4185
Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys	865	870	875 880	
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC				4233
Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro	885	890	895	
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT				4282
Gln Arg Met Phe Ile Thr	900			
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA				4330
Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys	905	910		
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT				4378
Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser	915	920	925 930	
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC				4432
Ala Glu Val Lys Trp	935			
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA				4480
Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys	940	945	950	
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT				4528
Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr	955	960	965	
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA				4576
Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu	970	975	980	
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC				4624
His Arg Arg Ile Ala Asp	985			
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC				4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC				4744

TFTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCA 4804
TAAACGGGA GTGGTTAAAC ATTAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA 4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT 4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT 4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG 5044
TGACCGAATT TTGGTAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG 5104
AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT 5164
GTTTTTCTCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA 5224
TTCCGAAATA GCCAAATTTT TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC 5284
TTATGAGGCT TCAAAAATC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT 5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTG CAAAAAAGAA AATATCATTG 5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT 5464
AACTTCTATT TCTGAAATGT ATGGTCTTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA 5524
GTTAAGTGAC CAAAGGTACC 5544

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 988 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
1 5 10 15
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
20 25 30
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
35 40 45
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
50 55 60
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
65 70 75 80
Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe
85 90 95
Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser
100 105 110
Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn

115					120					125					
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser
130						135					140				
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His
145					150					155					160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn
				165					170					175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu
		180						185					190		
Glu	Thr	Val	Ser	Lys	Lys	Arg	Lys	Arg	Thr	Ile	Glu	Thr	Ser	Ile	Thr
		195					200						205		
Gln	Asn	Lys	Ser	Ala	Arg	Lys	Glu	Val	Ser	Trp	Asn	Ser	Ile	Ser	Ile
	210					215					220				
Ser	Arg	Phe	Ser	Ile	Phe	Tyr	Arg	Ser	Ser	Tyr	Lys	Lys	Phe	Lys	Gln
225					230					235					240
Asp	Leu	Tyr	Phe	Asn	Leu	His	Ser	Ile	Cys	Asp	Arg	Asn	Thr	Val	His
				245					250					255	
Met	Trp	Leu	Gln	Trp	Ile	Phe	Pro	Arg	Gln	Phe	Gly	Leu	Ile	Asn	Ala
		260						265					270		
Phe	Gln	Val	Lys	Gln	Leu	His	Lys	Val	Ile	Pro	Leu	Val	Ser	Gln	Ser
	275						280					285			
Thr	Val	Val	Pro	Lys	Arg	Leu	Leu	Lys	Val	Tyr	Pro	Leu	Ile	Glu	Gln
	290					295					300				
Thr	Ala	Lys	Arg	Leu	His	Arg	Ile	Ser	Leu	Ser	Lys	Val	Tyr	Asn	His
305					310					315					320
Tyr	Cys	Pro	Tyr	Ile	Asp	Thr	His	Asp	Asp	Glu	Lys	Ile	Leu	Ser	Tyr
				325					330					335	
Ser	Leu	Lys	Pro	Asn	Gln	Val	Phe	Ala	Phe	Leu	Arg	Ser	Ile	Leu	Val
			340					345					350		
Arg	Val	Phe	Pro	Lys	Leu	Ile	Trp	Gly	Asn	Gln	Arg	Ile	Phe	Glu	Ile
		355					360					365			
Ile	Leu	Lys	Asp	Leu	Glu	Thr	Phe	Leu	Lys	Leu	Ser	Arg	Tyr	Glu	Ser
	370					375					380				
Phe	Ser	Leu	His	Tyr	Leu	Met	Ser	Asn	Ile	Lys	Ile	Ser	Glu	Ile	Glu
385					390					395					400
Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	Met	Cys	Leu	Ser	Asp
				405					410				415		
Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe	Ile	Tyr	Trp	Leu	Tyr
		420					425					430			
Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu
		435					440					445			

Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780

Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTT TYTAYNNNAC NGA

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
 1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2..3

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACCTT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACCTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAATA TTGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCTT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAGA TAGGATACTC AGTCTTTGAT AATAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1				5					10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
			20					25					30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
		35					40					45			
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
		50				55					60				
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65					70					75				80	
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
				85					90					95	
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
			100				105						110		
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
		115					120					125			
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys

130 135 140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
 1 5 10 15

Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
 20 25 30

Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
 35 40 45

Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
 50 55 60

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
 65 70 75 80

Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
 85 90 95

Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
 100 105 110

Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
 115 120 125

Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
 130 135 140

Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
 1 5 10 15
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
 20 25 30
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
 35 40 45
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
 50 55 60
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 65 70 75 80
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu
 85 90 95
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp
 100 105 110
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr
 115 120 125
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe
 130 135 140
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
 1 5 10 15
 Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
 20 25 30
 Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
 35 40 45
 Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp
 50 55 60
 Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys
 65 70 75 80
 Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys
 85 90 95

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val
100 105 110

Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val
115 120 125

Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys
130 135 140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
20 25 30

Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
35 40 45

Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
50 55 60

Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
65 70 75 80

Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
85 90 95

Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
100 105 110

Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
115 120 125

Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
130 135 140

Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
145 150 155 160

Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
165 170 175

Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
180 185 190

Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655
 Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln
 660 665 670
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn
 675 680 685
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys
 690 695 700
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr
 705 710 715 720
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln
 725 730 735
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu
 740 745 750
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu
 755 760 765
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu
 770 775 780
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile
 785 790 795 800
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln
 805 810 815
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp
 820 825 830
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly
 835 840 845
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu
 850 855 860

Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
865 870 875 880

Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
885 890 895

Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
900 905 910

Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
915 920 925

Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
930 935 940

Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
945 950 955 960

Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
965 970 975

Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe
980 985 990

Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
995 1000 1005

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 22..1716
 (D) OTHER INFORMATION: /note= "EcoRI-NotI insert of
 clone 712562 encoding 63 kDa

telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC TGC	ACTGGCT GAT	GAGTGTG TAC	GTCTCGTCG AGCT	GCTCTTCTTT	60
TATGTCACGG AGA	CACGTT TCAAA	AGAAG AGGCT	CTTTT TCTAC	CGGAA GAGT	120
GAGTGTCTGG					
AGCAAGTTGC AA	AGCATTGG AAT	CAGACAG CACT	TGAAGA GGGT	GTCAGCT GCGG	180
GAGCTG					
TCGGAAGCAG AG	GTCAGGCA GC	ATCGGGAA GCC	AGGCCCCG CCCT	GCTGAC GTCC	240
AGACTC					
CGCTTCATCC CCA	AGCCTGA CGG	GCTGCGG CCGA	TGTGA ACAT	GGACTA CGTC	300
GTGGGA					
GCCAGAACGT TCC	GCAGAGA AA	AGARGGCC GAG	CGTCTCA CCT	CGAGGGT GA	360
AGGCACTG					
TTCAGCGTGC TCA	ACTACGA GCG	GGCGCGCG CGC	CCCCGGCC TCCT	GGGCGC CTCT	420
GTGCTG					
GGCCTGGACG AT	ATCCACAG GGC	CTGGCGC ACCT	TTCGTGC TGC	GTCGTCG GGC	480
AGGAC					
CCGCCGCCTG AG	CTGTACTT TGT	CAAGGTG GAT	GTGACGG GCG	GTACGA CACC	540
ATCCCC					
CAGGACAGGC TC	ACGGAGGT CAT	CGCCAGC ATCAT	CAAAC CCC	AGAACAC GTAC	600
TGCGTG					
CGTCGGTATG CCG	TGGTCCA GA	AGGCCGCC ATG	GGCACGT CCG	CAAGGCC TTCA	660
AAGAGCC					
ACGTCCTACG TCC	AGTGCCA GGG	GATCCCCG CAG	GGCTCCA TCCT	TCTCCAC GCT	720
GTCTCTG					
AGCCTGTGCT ACG	GCGACAT GG	AGAACAAG CTG	TTTGCGG GGAT	TGCGG GGAC	780
GGGCTG					
CTCCTGCGTT TGG	TGGATGA TTT	CTTGTTG GTG	GACACCTC ACCT	CACCCA CGCG	840
AAAACC					
TTCTCAGGA CC	CTGGTCCG AGG	TGTCCCT GAG	TATGGCT GCG	TGGTGAA CTT	900
GCGGAAG					
ACAGTGGTGA ACT	TCCCTGT AGA	AGACGAG GCC	CTGGGTG GCAC	GGCTTT TGT	960
TCAGATG					
CCGGCCCACG GC	CTATTCCC CTG	GTGCGGC CTG	CTGTGCTG ATAC	CCGGAC CCT	1020
TGGAGGTG					
CAGAGCGACT ACT	CCAGCTA TG	CCCCGACC TCC	ATCAGAG CCAG	TCTCAC CTT	1080
CAACCGC					
GGCTTCAAGG CTG	GGAGGAA CAT	GCGTCGC AAAC	TCTTTG GGGT	CTTGCG GCT	1140
GAAGTGT					
CACAGCCTGT TT	CTGGATTT GC	AGGTGAAC AGC	CTCCAGA CCGT	GTGCAC CAAC	1200
ATCTAC					
AAGATCCTCC TG	CTGCAGGC GT	ACAGGTTT CAC	GCATGTG TGCT	GCAGCT CCC	1260
ATTTCAT					
CAGCAAGTTT GGA	AGAACCC ACAT	TTTTTCC TGC	GCGTCAT CTCT	GACACG GCT	1320
CCCTCTG					
CTACTCCATC CT	GAAAGCCA AGA	ACGCAGG GAT	GTGCTGCT GGG	GCCAAGG GCG	1380
CCCGCGG					
CCCTCTGCCC TCC	GAGGCCG TGC	AGTGGCT GTG	CCACCAA GCAT	TCTCTGC TCA	1440
AGCTGAC					
TCGACACCGT GT	CACCTACG TG	CCACTCCT GGG	GTCACCTC AGG	ACAGCCC AGAC	1500
CGCAGCT					
GAGTCGGAAG CT	CCCCGGGA CG	ACGCTGAC TG	CCCTGGAG GCC	GCAGCCA ACC	1560
CGGCACT					
GCCCTCAGAC TT	CAAGACCA TC	CTGGACTG ATG	GCCACCC GCC	CACAGCC AGG	1620
CCGAGAG					
CAGACACCAG CAG	CCCTGTC ACG	CCGGGCT TAT	ACGTCCC AGG	GAGGGAG GGG	1680
CGGCCCA					
CACCCAGGCC TGC	ACCGCTG GG	AGTCTGAG GC	CTGAGTGA GTG	TTTGGCC GAG	1740
GCCTGAGTGA					

TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA 1800
 GTGTCCAGCA CACCTGCGTT TTCACCTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC 1860
 CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG 1920
 ATTGCGCATT GTTCACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTCAGGT 1980
 GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGGAAATTTGG AGTGACCAA GGTGTGCCCT 2040
 GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCCTG TGGGTCAAAT TGGGGGGAGG 2100
 TGCTGTGGGA GTAAATACT GAATATATGA GTTTTTCAGT TTTGGAAAAA AAAAAAAAAA 2160
 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein encoded by ORF of EcoRI-NotI insert of clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
 1 5 10 15
 Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
 20 25 30
 Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
 35 40 45
 Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
 50 55 60
 Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
 65 70 75 80
 Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
 85 90 95
 Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
 100 105 110
 Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
 115 120 125

Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
 130 135 140
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
 145 150 155 160
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
 165 170 175
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
 180 185 190
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
 195 200 205
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 210 215 220
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 225 230 235 240
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 245 250 255
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 260 265 270
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 275 280 285
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 290 295 300
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 305 310 315 320
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460

Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480

Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495

Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510

Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525

Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540

Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560

Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTT TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
 1 5 10 15
 Tyr Arg Lys Ser Val Trp Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
 1 5 10 15
 Val Arg Gln His Arg Glu Ala
 20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 1 5 10 15
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
1 5 10 15

Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly
1 5 10 15

Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Thr Lys Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
1 5 10 15

Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
20 25 30

Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40 45

Asp Asp Tyr Leu Leu Ile Thr
50 55

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
1 5 10 15

Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
20 25 30

Val Val

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
1 5 10 15

Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
20 25 30

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Lys Val Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG

60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG

120

TAGTCGACGA CTACCTCCTC ATCACC

146

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe
1 5 10 15
Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys
20 25 30
Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr
35 40 45

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GACGATTTC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Asp Phe Leu Phe Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAAAAAAAAA AAAAAA

16

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTTTTTTTTT TTTTTT

17

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	
Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
			20					25					30		
Asp	Ile	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10				15		

Asn Leu Arg Lys Arg Phe
20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..26
 (D) OTHER INFORMATION: /note= "motif 3(A) peptide from
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..32
 (D) OTHER INFORMATION: /note= "motif 4(B') peptide from
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
20 25 30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn	Glu	Phe	Arg	Ile
1				5					10					15	
Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp							
			20					25							

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile
1				5					10					15	
Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..32

(D) OTHER INFORMATION: /note= "motif 4(B') peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1				5				10						15	
Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: /note= "motif 5(C) peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser	Thr	Asp	Gln
1			5					10						15	
Gln	Gln	Val	Ile	Asn	Ile	Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys
		20						25					30		
Tyr	Asn	Ala	Lys	Ala	Asn	Arg	Asp	Lys	Ile	Leu	Ala	Val	Ser	Ser	Gln
	35						40					45			
Ser															

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: /note= "motif 0 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 20 25 30
Asn Ile Trp
 35

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15
Thr Phe Asn Lys Lys Ile Val
 20

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..26
 (D) OTHER INFORMATION: /note= "motif 3(A) peptide from
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
1 5 10 15

Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15
Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu
1 5 10 15
Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu
20 25 30
Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln
1 5 10 15

Lys Ser Tyr Ser Lys Thr
20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys
1 5 10 15

Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif A peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15

Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala
20 25

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 22

(D) OTHER INFORMATION: /note= "motif C peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile
1 5 10 15

Thr Thr Gln Glu Asn Asn
 20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser
1 5 10 15

Asp Leu Arg Asn Arg Thr
 20

(2) INFORMATION FOR SEQ ID NO:155:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu
20 25 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

[illegible]

Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

97

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile
1 5 10 15
Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile
1 5 10 15
Thr Val Asn Lys Lys Asp
 20

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..22
 - (D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
 1 5 10 15
 Ser Thr Val Thr Ile Val
 20

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..32
 - (D) OTHER INFORMATION: /note= "motif 0 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
 1 5 10 15
 Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro	Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser
1				5				10						15	
Ile	Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys					
			20					25							

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Glu	Asp	Lys	Cys	Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser
1				5					10					15	
Leu	Ser	Ala	Pro	Ile	Val	Asp	Leu	Val	Tyr	Asp					
				20				25							

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
1 5 10 15
Ser Thr Asp Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide.
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide.
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif 1 peptide from human
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
1 5 10 15
Phe Gln Lys Asn Arg Leu
20

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5 10 15
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
1 5 10 15
Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile
1 5 10 15

Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
20 25

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..22

(D) OTHER INFORMATION: /note= "motif C peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val
1 5 10 15

Thr Pro His Leu Thr His
20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY:
(B) LOCATION: 1..4029
(D) OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC 60
GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC AGCCACTACC GCGAGGTGCT 120
GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG 180
GGACCCGGCG GCTTTCCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN 240
ANGGCNGCCC CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC 300
CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC 360
GCTGCTGGAC GGGGCCCCGCG GGGGCCCCC CGAGGCCTTC ACCACCAGCG TGCGCAGCTA 420
CCTGCCCAAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG 480
CCGCGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TGC GCGNTNT TTGTGCTGGT 540

GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTTGGAG	GGTGCGCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCCA	1200
GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGCCC	1260
CTACGGGGTG	TTCTCAAGA	CGCACTGCCC	GCTGCGAGCT	GCGGTCACCC	CAGCAGCCGG	1320
TGTCGTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTCTG	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560
CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTGCGAAG	1860
CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCGTG	GGAGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTCAGCG	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA	2400

GECCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG	2460
GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCGCATC AGGGGCAAGT	2520
CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC	2580
TGTGCTACGG CGACATGGAG AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC	2640
TGCGTTTGGT GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC	2700
TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG CGGAAGACAG	2760
TGGTGAACCT CCCTGTAGAA GACGAGGCC TGGGTGGCAC GGCTTTTGTT CAGATGCCGG	2820
CCCACGGCCT ATTCCCCTGG TCGGCCTGC TGCTGGATAC CCGGACCCTG GAGGTGCAGA	2880
GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT	2940
TCAAGGCTGG GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTACA	3000
GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA	3060
TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT GCAGCTCCCA TTTCATCAGC	3120
AAGTTTGGAA GAACCCACA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT	3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC	3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC	3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG ACGCAGCTGA	3360
GTGCGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC	3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC	3540
CCAGGCCCCG ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCAGGGCC	3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTGCCATTG TTCACCCCTC GCCCTGCCCT CTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAA AAAAAAAA	4020
AAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1 5 10 15
Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20 25 30
Ala Gln Pro Leu Pro Arg Gly Ala Ala Ala Gly His Val Arg Ala Ala
35 40 45
Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50 55 60
Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa
65 70 75 80
Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu
85 90 95
Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu
100 105 110
Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly
115 120 125
Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His
130 135 140
Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala
145 150 155 160
Pro Arg Gly Arg Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa
165 170 175
Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala
180 185 190
Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg
195 200 205
Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala
210 215 220
Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu
225 230 235 240
Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln
245 250 255
Ala Trp Arg Cys Pro
260

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln
 1 5 10 15
 Asp Ala Trp Thr Glu
 20

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
 1 5 10 15
 Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
 20 25 30
 Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
 35 40 45
 Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
 50 55 60
 Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
 65 70 75 80
 Tyr Ile

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
 1 5 10 15
 Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
 20 25 30
 Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
 35 40 45
 Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
 50 55 60
 His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
 65 70 75 80
 Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
 85 90 95
 Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
 100 105 110
 Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
 115 120 125
 Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
 130 135 140
 Ser Met Pro Ser Ser Arg Cys Arg Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
 1 5 10 15
 Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser
 20 25 30
 Cys Thr Gly
 35

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg
1 5 10 15
Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly
20 25 30
Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr
35 40

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile
1 5 10 15
Gly Lys Pro Gly Pro Pro Cys
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
1 5 10 15

Pro Ser Val Ser Pro Arg Gly
20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1 5 10 15

Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
20 25 30

Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
35 40 45

Thr Leu Ser Arg Trp Met
50

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1 5 10 15

Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
20 25 30

Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
35 40 45

Thr Ser Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
 1 5 10 15

Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
 1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
 20 25 30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
 35 40 45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
 50 55 60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp
 65 70

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
20

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Thr Cys Gly Arg Gln Trp
1 5

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
50 55 60

Ser Leu Gly Ser Cys Gly
65 70

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
1 5 10 15
Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser
20 25 30
Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg
35 40 45
Pro Pro Ser Ala Thr Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
 20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
 1 5 10 15

Pro Arg Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Val Gly Ser Ser Arg Gly Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
 1 5 10 15

Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
 20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
 35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Leu Ser Glu Cys Pro Ala Lys Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg
 1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu
 20 25 30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
 20 25 30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
 35 40 45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50 55 60

Ala Val Gly Val Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
 20 25 30
 Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
 35 40 45
 Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
 50 55 60
 Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
 65 70 75 80
 Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
 85 90 95
 Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
 100 105 110
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 115 120 125
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 130 135 140
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 145 150 155 160
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
 165 170 175
 Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
 180 185 190
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 195 200 205
 Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
 1 5 10 15
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 20 25 30
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
 50 55 60
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 65 70 75 80
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 85 90 95
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
 100 105 110
 Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
 115 120 125
 Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
 130 135 140
 Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
 145 150 155 160
 Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
 165 170 175
 Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
 180 185 190
 His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
 195 200 205
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
 210 215 220
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser
 225 230 235 240
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
 245 250 255
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
 260 265 270
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg
1 5 10 15
Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys
20 25 30
Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys
35 40 45
His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val
50 55 60
Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp
65 70 75 80
Val Gln Thr Pro Leu His Pro Gln Ala
85

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn
1 5 10 15
Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly
20 25 30
Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro
35 40 45
Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His
50 55 60
Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15
Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 30
His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45
Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60
Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80
Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15
Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30
Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45
His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60
Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
 1 5 10 15
 Asp Pro Gly Pro Arg Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
 1 5 10 15
 Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
 20 25 30
 Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
 35 40 45
 Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
 50 55 60
 Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
 65 70 75 80
 Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
 85 90 95
 Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
 100 105 110
 Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile
 115 120 125
 Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp

1	5	10	15												
Val	Ala	Gly	Gly	Gln	Gly	Arg	Arg	Arg	Pro	Ser	Ala	Leu	Arg	Gly	Arg
		20						25					30		
Ala	Val	Ala	Val	Pro	Pro	Ser	Ile	Pro	Ala	Gln	Ala	Asp	Ser	Thr	Pro
		35					40					45			
Cys	His	Leu	Arg	Ala	Thr	Pro	Gly	Val	Thr	Gln	Asp	Ser	Pro	Asp	Ala
	50					55					60				
Ala	Glu	Ser	Glu	Ala	Pro	Gly	Asp	Asp	Ala	Asp	Cys	Pro	Gly	Gly	Arg
65					70					75					80
Ser	Gln	Pro	Gly	Thr	Ala	Leu	Arg	Leu	Gln	Asp	His	Pro	Gly	Leu	Met
				85					90					95	
Ala	Thr	Arg	Pro	Gln	Pro	Gly	Arg	Glu	Gln	Thr	Pro	Ala	Ala	Leu	Ser
			100					105					110		
Arg	Arg	Ala	Leu	Arg	Pro	Arg	Glu	Gly	Gly	Ala	Ala	His	Thr	Gln	Ala
		115					120					125			
Arg	Thr	Ala	Gly	Ser	Leu	Arg	Pro	Glu							
		130				135									

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Val	Phe	Gly	Arg	Gly	Leu	His	Val	Arg	Leu	Lys	Ala	Glu	Cys	Pro	Ala
1				5				10					15		
Glu Ala															

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala	Ser	Val	Gln	Pro	Arg	Ala	Glu	Cys	Pro	Ala	His	Leu	Pro	Ser	Ser
1				5				10					15		

Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro
 20 25 30
 His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro
 35 40 45
 Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro
 50 55 60
 Pro Pro Ser Arg Trp Arg Pro
 65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro
 1 5 10 15
 Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser
 20 25 30
 Asn Trp Gly Glu Val Leu Trp Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys
 1 5 10 15
 Lys Lys

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro
1 5 10 15
Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys
20 25 30
Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala
35 40 45
Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu
50 55 60
Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa
65 70 75 80
Gly Xaa Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala
85 90

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg
1 5 10 15
Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly
20 25 30
Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
 1 5 10 15
 Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
 20 25 30
 Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
 35 40 45
 Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
 50 55 60
 Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
 65 70 75 80
 Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
 85 90 95
 Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
 100 105 110
 Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
 115 120 125
 Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
 130 135 140
 Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
 145 150 155 160
 Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175
 Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190
 Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
 195 200 205
 Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220
 Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335

Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670

Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 805 810 815
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 820 825 830
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 835 840 845
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 850 855 860
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
1 5 10 15
His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
 20 25 30
Pro Ala Pro Leu Gly Val
 35

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
1 5 10 15
Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
 20 25 30
Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
 35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
85 90

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Val Phe Gln Phe
1

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GCAGCGCTGC	GTCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106						
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
5 10 15							
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154						
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro							
20 25 30							
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202						
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala							
35 40 45							
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250						
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro							
50 55 60 65							
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298						
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val							
70 75 80							
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346						
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu							
85 90 95							
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394						
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu							
100 105 110							
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442						
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp							
115 120 125							

GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	1210

370					375					380					385	
TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
				390					395					400		
CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
			405					410					415			
GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
		420				425					430					
TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
	435				440						445					
CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
450				455				460							465	
CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
				470				475						480		
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
			485					490					495			
GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
	500					505						510				
GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
	515					520					525					
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
530				535				540							545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
				550				555						560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
			565					570					575			
AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
		580				585						590				
AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
	595					600					605					
CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
610					615					620					625	

AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys	2698

GEA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG 3471
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA 3531

GGGGCGGCCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTTGGC 3591

CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG 3651

CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCCTCGGC 3711

TCCACCCCAG GGCCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT 3771

AGTCCATCCC CAGATTGCGC ATTGTTTACC CCTCGCCCTG CCCTCCTTTG CCTTCCACCC 3831

CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC 3891

AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA 3951

AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA 4011

AAAA 4015

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140

Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190	
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220	
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	225	230	235	
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	245	250	255	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	260	265	270	
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	275	280	285	
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	290	295	300	
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	305	310	315	
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	325	330	335	
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	340	345	350	
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	355	360	365	
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	370	375	380	
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	385	390	395	
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	405	410	415	
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	420	425	430	
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	435	440	445	
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	450	455	460	
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	465	470	475	
																480			

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130